REMARKS

Reconsideration is requested.

Claims 10, 11 and 13-20, defining non-elected subject matter, have been canceled above, to advance prosecution.

Claims 1-9, 12 and 21 are pending.

The specification has been revised to delete embedded hyperlinks and other forms of browser-executable code. The specification has been revised to capitalize the term indicated as being a Trademark and provide a generic description of the same. Withdrawal of the objections to the specification stated on page 3 of the Office Action dated September 21, 2007 is requested.

The claims have been amended, without prejudice, to advance prosecution. Support for the claim revisions is believed to exist in the originally-filed application. Specifically, for example, basis for the revision to claim 1 with regard to the identity of the protein may be found in the unamended claim 1 as well as on page 2, line 14-18: page 3, lines 5-6, page 4, line 33 to page 5, line 3; page 26, lines 14-15; page 6, lines 35-37 and on page 30. line 15 to page 33, line 6. The claims have also been revised to refer to control plants, as opposed to wild type plants, as described, for example, on page 15, line 16; page 32, line 5 and page 33, lines 23-24 of the specification. No new matter has been added. Claim 21 has been added to define further

The Section 112, second paragraph, rejection of claims 1-9 and 12 is believed to be obviated by the above amendments. For completeness, the applicants note that TOB3 was a known term at the time of filing (see attached printouts of AF34078 (human TOB3) and AAK38648 (mouse TOB3). Moreover, it was also known that T0B3 belongs

- 11 -

to the AAA-ATPase family (see attached GenBank entry AF343078). Reconsideration
and withdrawal of the rejection are requested.

To the extent not obviated by the above amendments, the Section 112, first
paragraph "written description", rejection of claims "1, 2, 4 and 7-19" is traversed. (The
Examiner perhaps intended to only reject claims 1, 2, 4 and 7-9 however clarification is
requested if otherwise.) Reconsideration and withdrawal of the rejection are requested
in view of the above and the following further comments.

The description on page 3, lines 5-6, discloses that the TAD protein comprises
an ATPase domain. Moreover, on page 4, line 33 to page 5, line 4, it is disclosed that
the homologues have in increasing order of preference at least 70%. 80%. 85%, 90%,
95% 96%, 97%. 98% or 99% sequence identity. An alternative definition (page 5, lines
6-9) states that the homologues have ATP binding and/or ATPase activity, and
comprise a sequence of 22 consecutive ammo acids having at least 90% sequence
identity to a corresponding sequence in SEQ ID NO:2. The homologues of a TAD
protein also encompass sequences that hybridize under stringent conditions to SEQ ID
NO:1 (page 7, line 10-12). Stringent hybridization conditions are defined, for example,
on page 8, line 10 to 31. Moreover, the applicants believe that a number of homologues
to SEQ ID NO:2 are described on page 3, lines 20 to 23.

The claims are submitted to be supported by an adequate written description.
Withdrawal of the Section 112, first paragraph, rejection of claims "1, 2, 4 and 7-19" is
requested.

The Section 112, first paragraph "enablement", rejection of claims 1-9 and 12 is
believed to be obviated by the above amendments. The claims are submitted to be

- 12 -

supported by an enabling disclosure. Many of the concerns raised by the Examiner in the rejection have been obviated by the above amendments and withdrawal of the Section 112, first paragraph "enablement", rejection of claims 1-9 and 12 is requested.

The Section 102 rejection of claims 1, 2 and 4-9 over Lorenzo (January, 2002, Plant Cell Physiology 43:27-34), is traversed. Reconsideration of the rejection are requested in view of the following distinguishing comments.

The applicants believe that the sequence of FsA1, disclosed by the cited art only has 22 8% sequence identity to SEQ ID NO:2 (that is when the corresponding sequences are compared, when the full length of FsA1 is compared with SEQ ID NO:2, then the sequence identity is less than 14%, see alignments attached as Annex 2).

The cited art is therefore not believed to anticipate the claimed invention which requires a minimum of 70% sequence identity to SEQ ID NO:2.

Withdrawal of the Section 102 rejection is requested.

The Section 102 rejection of claims 1-3, 8, 9 and 12 over Kwart (U.S. Patent Application Publication No. 2004/0168214), is traversed. Reconsideration and withdrawal of the rejection are requested in view of the attached alignment (see Annex 3) between SEQ ID NO:2 and the PHA2 protein sequence. Moreover, the cited reference is believed to be related to increased biomass, as opposed to see yield, as presently claimed.

Withdrawal of the Section 102 rejection is requested.

The claims are submitted to be in condition for allowance and a Notice to that effect is requested. The Examiner is requested to contact the undersigned in the event anything further is required in this regard.

1285758

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____/B. J. Sadoff/_____
B. J. Sadoff
Reg. No. 36,663

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Arlington, VA 22203-1808
Telephone: (703) 816-4000
Facsimile: (703) 816-4100

1285758

Annex 1: AF34078 (human TOB3) and AAK38648 (mouse TOB3)

```
ID   AF34078    standard; RNA; HUM; 1966 BP
XX
AC   AF343078;
XX
SV   AF343078.1
XX
DT   26-APR-2001 (Rel. 67, Created)
DT   26-APR-2001 (Rel. 67, Last updated, Version 1)
XX
DE   Homo sapiens TOB3 mRNA, complete cds.
XX
XX
KW   .
XX
OS   Homo sapiens (human)
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia;
OC   Eutheria; Primates; Catarrhini; Hominidae; Homo.
XX
RN   [1]
RP   1-1966
RA   Parng C., Piepenhagen P.A., Casanova J., Pillai S.;
RT   "TOB3 is a novel AAA-ATPase involved in protein secretion";
RL   Unpublished.
XX
RN   [2]
RP   1-1966
RA   Parng C., Piepenhagen P.A., Casanova J., Pillai S.;
RT   ;
RL   Submitted (26-JAN-2001) to the EMBL/GenBank/DDBJ databases.
RL   The MGH Cancer Center, Massachusetts General Hospital, Building 149, 13th
RL   St., Charlestown, MA 02139, USA
XX
DR   ENSEMBL1; ENSG00000160072; ENST00000308647
DR   GOA; Q96T67; O9GT67.
DR   SPTREMBL; Q96T67; Q96T67.
XX
FH   Key             Location/Qualifiers
FH
FT   source          1..1966
FT                   /chromosome="1"
FT                   /db_xref="taxon:9606"
FT                   /organism="Homo sapiens"
FT                   /dev_stage="embryo day 16"
FT   CDS             67..1803
FT                   /codon_start=1
FT                   /db_xref="GOA:Q96T67"
FT                   /db_xref="SPTREMBL:Q96T67"
FT                   /note="member of AAA-ATPase family"
FT                   /product="TOB3"
FT                   /protein_id="AAK38647.1"
FT                   /translation="MSWLFGIKGPKGEGAGPPPPLPPAQPGAEGGGDRGLGDRPAPKDK
FT                   WSNPDDTCLERAAKAARELHFGRYAKDALNLAQMGEQTLQLRQQSKLKEYRAAVEQLKS
FT                   EGIRAAEERRKTLSEETRQNQARAGYQDKLAKGRYEDQLKQQQLLNEENLRKOEESVQ
FT                   KQGAMRRATVERRMELRHKNEMLKVFARRAEAKAEERENADIIREQIRLKASEHRQTVL
FT                   ESIRTAGTLFGEGFRAFVTEWDKVTATVAGLTLLAVCVYSAKNATLVAGKYIKARLGKP
FT                   SIVRETSRLTVLEALRHPIQVSERSRLSPRPQDALEGVVLSPSLEARVRDIAIATLNTVKN
FT                   RSLPRNILMYGPPCPCKTLFAKKLPLIISGMDYAIMIGGDVAPMGGKGVTAMHKLFDWAN
FT                   TSRRGLLLFMDEADAFLRKRATEEISKDLRAYLNAPLYHMGQHSNKFMLVLASNLPEQF
FT                   DCAINSKIDVMVHFDLPQQKRREPWVRLHFDNCVLKPATEGKQRLKLAQFDYGRKCSEV
FT                   AKLTECMSCREIAQLAVSWQATAYAGEDGVLTEAMMDTRVQDAVQQHQQKMCWLKAECS
FT                   LC"
XX
SO   Sequence 1966 BP; 418 A; 569 C; 683 G; 291 T; 5 other;
     ccagccgcgc gcgagtcaga ctcuguguug ggtcccggcg gcggtgggca cggcggcaat        60
     gcgagccatgt cgtggctcct cggcatcaag ggccccaagg gtgaaggcgc ggggccgcca       120
```

```
       ccgcctttgc cgcccgcgca gccgcagggcc gagggcggcg gggaccgcgg gttgggagac    180
       cgcccgcgc ccaagtacca atggcgcaac ttcgaccca ccggcccgga gcgcgccgcc       240
       aaggcgggcgc gcgagctgga gcgctcgcgt catgccaagg acgcccgaa tctggacag       300
       atgcaggagc agacgctgca gttggagcaa cagtccaacg aaggcaaggt tgggccgct       360
       gtcggcagac tcaagagcga gcagatccgg gcgcaggctg aggagggagg gaagaccctg       420
       agggggtgcg ccggccgca ccaggccagg gcccagtacc aggcaaagct ggcccgccag       480
       cgctacgagg accaactgaa gcagcagcaa cttctcaatg aggagaattc acggcagcag       540
       gaggagtccg tgcagaagca ggaagccatg cagcaagca.a agtggagcg gaggatggag       600
       ctgccggcca agaatgagat gctgcgagtg gaggcgggg cccgggcgcg cgccaaggcc       660
       gagcgggagc atgcagacat catccgcgag cagctcgcc tgaaggccgc cgagcaccgt       720
       cagacggtct tggagtccat caggagcggct ggcacctgt ttgggaaga atccgtgcc       780
       tttgtgacag actgggacaa agtgacagcc aaggtggtcc gaccgctgct gctgggtgtt       840
       gggttctact cagccaagaa tgccacgctt gtcgcccggcc gcttcatcaa agcttcggctg       900
       gggaagccgt cccatgcagg ggagacgtcc cgcataccgg tacttgaggc gctgcggcac       960
       cccatccaag tcaagccgtc tcgtctcagt cgacccaagg acgcgttgga gggtgttgtg      1020
       cccagtccca gcctggaagc acggtgcgc gacatcgcca tagcaacttt gaacaccaag      1080
       aagaacgagc gcctgttcag gaacattctg atgcacggg cacaggccc cggagaggcg      1140
       ctgtttgcca agaaacttcc cctgcactca ggcatggaac acgcatcat gacaggcggg      1200
       gacgtggccc ccatgggggg gaaaggcgtg aacgccatgc acaagctcct tgacggggcc      1260
       aataccaagc gagagggctt cctgctcttc atggtgaag cagacgcctt cctccggaag      1320
       cgagccacta aggagatuug caaggacctc agagccacac tgaacgcctt cctgtaccac      1380
       acgggccaac acagcaacaa atccatgctg gcccaggcca gcaatctgc tgagcagttc      1440
       gactggtgca tcaacaccca cattgaggtg ctggtcccct ccgacctgcc ggacgcagaag      1500
       gagcgggagc cctcagcagg actgcccttt gacaacgctg tccttaagcc ggccacaaaa      1560
       ggaaagcagc gcctgaagct ggcccagttc gactacggga ggaagctagtc agaggtcgct      1620
       cggctgacgg agggcatgtc gggcgggag atcgctcagc cgacggtgtc ctggccaggcc      1680
       acggcgtacg cgtccaggga cgggtcctg acggagggcc tgatggacac ccgcgtgcag      1740
       gatgctgtca agagtuuct gcggaggata tgctggctga agggcggaag atcgctcggc      1800
       tgaaagggg cctgtaatgc cggaaggatg cacagcrggc catgtcctgg caggccacgg      1860
       cgtatgttcc aaggacggga tcctgaccga ggrcatgatg cacgcctgct tgcaagattt      1920
       tctccagcag caccagcaga tgctgcgcctg gctgaaggg gagagg                  1966
//
```

```
LOCUS       AF343079                1941 bp    mRNA    linear   ROD 23-APR-2001
DEFINITION  Mus musculus TOB3 mRNA, complete cds.
ACCESSION   AF343079
VERSION     AF343079.1  GI:13752412
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1941)
  AUTHORS   Pareng,C., Piepenhagen,P.A., Casanova,J. and Pillai,S.
  TITLE     TOB3 is a novel AAA-ATPase involved in protein secretion
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1941)
  AUTHORS   Pareng,C., Piepenhagen,P.A., Casanova,J. and Pillai,S
  TITLE     Direct Submission
  JOURNAL   Submitted (26-JAN-2001) The MGH Cancer Center, Massachusetts
            General Hospital, Building 149, 13th St., Charlestown, MA 02129,
            USA
FEATURES             Location/Qualifiers
     source          1..1941
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="BALR/c"
                     /db_xref="taxon:10090"
     CDS             142..1917
                     /note="member of AAA-ATPase family"
                     /codon_start=1
                     /product="TOB3"
                     /protein_id="AAK38648.1"
                     /db_xref="GI:13752413"
                     /translation="MSWLPGIKCPKCEGTGPPLPLPFAQPGAEGGGDRGAGDRPSPKD
                     KWSNFDPTGLERAAKAARELEHSRHAKEALSLAQMPQTLQLEQQESKLKEYEAAVEQL
                     KSEQIRVQABERRKTLTEETRQHQARAQYQDKLARQRYEDQLKQQOLLNEENLRKQEE
```

SVQKQEAIRRATVEREMELRHKNEMLRVEAEARARAKADRENADIIRFQIRLKAAEHR
QTILEGIRTAGTLLGEGFRAFVTDWDKVTATVAGLTLLAVCVYSAKNATGVAGRYIEA
RLGKPSLVRETSKISVLEALRHPTQVSSRRLVSRPQDALEGVILQPSLEARVRDIAIAT
RNTKNKSLYRNVLMYCPGTGKTLFAKKLALHSGMDYAIMTGGDVAFMGREGVTAMH
KVFDWASTSRRCLLLFVDDADAFLRIKRATEKISEDLRATILNAFLHKIUQHESKFMLVL
ASNQPEOFDWAINDRIDEMVCFALPQRREKERLVRMYFDKYVLKPATECKQRLKVAQF
DYGKKCSEVAQLTEGMSGREIAULAVAWQAMAYSEEDGVLTEAMMDARVODAVUQHQQ
KMQWLKVRRPDSQTNKPPHPSLLSC"

ORIGIN
```
   1 tnattagacg ctgnactncc tactaaatgc ccncctngat tgccattggc gaacccaccc
  61 cgttctggga cgtgggtggn ctgcnagaag cctcgtcggct cacgcccgg acggtccgcc
 121 gaggccgcgg agttgcagac catgtcgtgg ctcttcggca tcaagggccc caagggcgna
 181 ggcacggggc ctccgctgcc cttgccgccc gctcaacccg gggcggugg cggcggtgac
 241 cgcggggcgg gagaccggcc atcgccaang gacaaatgga gcaacttcga ccaacggag
 301 cfggaacgtg cggccaaagc ggctcgcgag ttggagcaac cgrgcratgc caaggugggca
 361 ctgagtctcg cacagatgca ggacgagacg ctcgcacttyg cacagcaatc caagctcaag
 421 gagtacgaag ctgccgtaga gcngcrgaag agcgaacaga tccgtgcgca agccgaagaa
 481 agaaggaaaa ccctgactga agagacacga cagccaccag ctagggccca gtaccaggat
 541 aagctccctc gacacgcgctu tgaggaccag ctgaaacaac agcaacttct gaatgaagag
 601 aacttaaggg aacagagga gtctgtgcag aagcaggagg ccatagggcg agccactgtg
 661 gagcgcgaga cggagctgag gcataaaaac gaungrgttgc gggtggaagc tgaagccaga
 721 gcacgggcca aggctgatcg agagaatgca gututcatcc gggaacagat tcgactcaag
 781 gctgctgngc aucgccagac catcttggac tctatcagga cagctggcac cttgcttggt
 841 ggaggattcc gtgcatttgt gacagactgg gacaaaatga cngctacggt ggctgggttg
 901 acocattag ctgttggagt ctactctgca aaggatgcta tttctgttgc tggtcggtat
 961 attgaggccc gattggaaaa gcagcgcrtg gtgagagaga cctcccgaat ctngtgcta
1021 gaggcattga ggcatccccut ccaggtcagc aggcgactgg tcagcagace ccaggatgca
1081 ttggagggcg tcacccctcag tcctagcctg gaagacggg tccgagatat tgccatcgca
1141 acaagaaata ccagaaagaa caaaagcctg tatatggaag ctttgatgta tgggccccctg
1201 ggactggcca aganacatatt tgccaagaaa ctggcactgc attcaggcat ggactacggc
1261 atcalgacag gcgggggcgt ggccccaatg gggcgggagg atgtgtcgc catgcacaag
1321 grettcgact gggcaagcac cagccgacga ggcctccctgc tctttgtgga tgragcagac
1381 gccttcctca gaaaacgagc gactgtnaag ataagcgag acctcaggac cactctgaat
1441 gccttcctac acaggacagg acagcacagt agcaagtten rgctgggcct ggccagtaac
1501 cngcctgagc agttttgactg ggctatcaat gaccgcattg acgagatggt ctgctttgcc
1561 ctgcccaccg gggaggaagg agagcgccrg gtgaagaagc atttggacaa gtatgtcccnt
1621 aagccggcca cagaaggaaa gcacgccttg aagagcgcc agtttgacta tggaaagaaa
1681 tgttcagagg ttgcccagct cacgggggg atgtcaggcc gggagattcc tcngcttgct
1741 gtggcgtggc aggccattgr atttcatct gaggatcgag tcctaacgga agctatgarg
1801 gatgccgtg tgcaggatgc tgtgcagcag caccagcaga agatgcagtg gcttaaagra
1861 gagagaccng attcccagac caacaagccg cccacatcctt cactcctcag ctgctgaget
1921 ggacttggac accttgcaca c
```
//

Annex 2: alignment of SEQ ID NO: 2 with FsA1 (full length and ATPase domain)

```
########################################
# Program:  needle
# Rundate:  Mon Dec 10 11:10:08 2007
# Align_format: srspair
# Report_file: outfile
#######################################
#=======================================
#
# Aligned_sequences: 2
# 1: SEQIDNO2
# 2: FsA1
# Matrix: EBLOSUM62
# Gap_penalty: 11.0
# Extend_penalty: 1.0
#
# Length: 470
# Identity:     63/470 (13.4%)
# Similarity:  108/470 (23.0%)
# Gaps:        274/470 (58.3%)
# Score: 158.0
#
#
#=======================================

SEQIDNO2           1                                                        0

FsA1               1  MALETKHPEAVPADETCSAKCSKQCEGLKQYYLQHIHDHQLQVRQKTHNI,    50

SEQIDNO2           1                                                        0

FsA1              51  NRLEAQRNEFNSRVRMLREZLQLLQEPGSYVGEVVKVMGKNKVLVKVHSE   100

SEQIDNO2           1                                                        0

FsA1             101  GKYVVDIDKNIDITKITPSTRVALRNDGYVLHLILPSKVDPLVNLMKVEK   150

SEQIDNO2           1                                              MLFYGP      6
                                                                   .|.|||
FsA1             151  VPDSTYDMIGGLDQQIKEIKEVIELPIKIPELFLESLGIAQPKGVLLYGP   200

SEQIDNO2           7  PGTGKTMVAREIARKSGLDYAMMTGGD-VAPLCAQAVTKIHEIFDWAKKS    55
                        ||||||:|:|.:|....    .|.:| |. ...:....|.|..|::
FsA1             201  PGTGKTLLARAVAHHTDCTFIRVGGSELVQKYIGEGSRMVRELFVMARE   249

SEQIDNO2          56  NKGLLLFIDEADAPLCER----NSTYMSEAQRFAINALLFRTGDOS-RDV   100
                        :....:|.|:|.| ....    :....||.|.|:.|...|:.|| :..
FsA1             250  HAPSIIFMDEIDSIGSARMESGGSGNGDSEVQDHMLELLNQLDGFESIKQT   299

SEQIDNO2         101  VLVLATNRPGDLDSAV--TDKIDEVIEFPLPQRFERPKLLKLY--LN--   143
                        .....||...||.|.   .||. .||| .|||.| |.|.|:|.    :|
FsA1             300  KVLMRTNRIDILDQALLRPCRIDRKIEFPNPNRESRFDILKTHSRRMNLM   349

SEQIDNO2         144  -----KYLAGEGDSDSNSKW------GHLFKKNQQKR---ITIODLSDDV   179
                        |:.|.... |....    ...|.....|   :|.|..|..|
FsA1             350  RGIDLKKIAEKMNDAGGAELKAVCTEAGMFALTAERKVRLVTQEDFFMAV   399

SEQIDNO2         180  IREAAKKIE-GPSGREIAKLMASVCATVYGSPDCVLDSQLFKEIVDYKVA   228
                        .|.| .|.|:.:|
FsA1             400  AKVMKKETEKNMSLKKLWK                                 418

SEQIDNO2         229  EHHQRIKLAARGMEPTYQGN    248

FsA1             419                            418

#----------------------------------  ----
```

```
#-------------------------------------

########################################
# Program: needle
# Rundate: Mon Dec 10 11:14:31 2007
# Align_format: srspair
# Report_file: outfile
########################################
#=======================================
#
# Aligned_sequences: 2
# 1: SEQIDNO2
# 2: FsAlpart
# Matrix: EBLOSUM62
# Gap_penalty: 11.0
# Extend_penalty: 1.0
#
# Length: 276
# Identity:      63/276 (22.8%)
# Similarity:   108/276 (39.1%)
# Gaps:          80/276 (29.0%)
# Score: 159.0
#
#
#=======================================


SEQIDNO2          1 MLFYGPPCTGKTMVARGIARKSGLDYAMMTGGD-VAPLGAQAVTKIHEIF     49
                      :|.|||||||:|:.|..........:....|.| .| .....:...: |.|
FsAlpart          1 VLLYGPPGTGKTLLARAVAHHTDCTFIRVSGGELVQKYIGEGSRMVRELF     50

SEQIDNO2         50 DWAKKSNKGLLLFIDEADAFLCER----NSTYMSEAQRSALNALLFRTGD     95
                      ..|::...|....|:|:|:|.||.   ....:||.|.||...|......:|.
FsAlpart         51 VMARE-HAPSIIFMDEIDSIGSARMESGSGNGDSEVQDHMLELLNQLDGF     99

SEQIDNO2         96 QS-RDVVLVLATNRPGDLDSAV--TDKIDEVIFFPLPQESERFKLLKLY-    141
                      :|.......||:|:|:|..|||:...||| |||.|.:|:|.::|:|:|.|.
FsAlpart        100 ESIKQIKVIMRTNRIDILDQALLRPGRIDRKIEFPNPNRESRFDILKIHS    149

SEQIDNO2        142    LN------KYLAGEGDSDSNSKN------GHLFKKNQQKR---ITIO    173
                         :|     |..:|.|.:..:.        ..|.|..::|.   |.:.
FsAlpart        150 RRMNLMRGIDLKKIAEKMNCASGCAELKAVCTDAGMFALTAERRVRLVTQE    199

SEQIDNO2        174 DLSDDVIREAAKKIE-GFSGREIAKLMASVQATVYGSPDCVLDSOLFKEI    222
                      |....|.:...|.|.|.| |.|
FsAlpart        200 DFEMAVAKVMKKETFKNMSLRKLWK                           224

SEQIDNO2        223 VDYKVAEHHQRIKLAAEGMEPTYQGN     248

FsAlpart        225                                  224


#    -------------------------------------
#-------------------------------------
```

Annex 3: alignment of SEQ ID NO: 2 with PHA2

```
#######################################
# Program:  needle
# Rundate:  Mon Dec 10 11:16:34 2007
# Align_format: srspair
# Report_file: outfile
#######################################
#=======================================
#
# Aligned_sequences: 2
# 1: SEQIDNO2
# 2: StPHA2
# Matrix: EBLOSUM62
# Gap_penalty: 11.0
# Extend_penalty: 1.0
#
# Length: 1160
# Identity:      8/1160 ( 0.7%)
# Similarity:   18/1160 ( 1.6%)
# Gaps:      1120/1160 (96.6%)
# Score: 20.0
#
#
# ====================================
```

SEQIDNO2	1 MLFYGPPGTGKTMVAREIARKSGLDYAMMTGGDVAPLGAQOAVTKIHEIPD	50
StPHA2	1	0
SEQIDNO2	51 WAKKSNKGLLLFIDEADAFLCFRNSTYMSEAORSALNALLFRTGDQHRDV	100
StPHA2	1	0
SEQIDNO2	101 VLVLAINRPUDLDSAVTDRIDEVIEFPLPQEEBRFKLLKLYLNKYLAGEG	150
StPHA2	1	0
SEQIDNO2	151 DSDSNSKWGHLFKIQNQQKRITIQDLSDDVIREAAKKIEGFSGREIAKLMA	200
StPHA2	1	0
SEQIDNO2	201 SVQATVYGSPDCVLDSQLFKRIVDYK---VAEHIQRIKLAAEGMFPTYQG	247
StPHA2	1 MAKAISLEDIKNETVDLEKIPTERVFEQLKCSREGLTSDEGA	42
SEQIDNO2	240 N	248
StPHA2	43 NRLQIFCFNKLEEKKESKILKFLGFMWNPLSWVMEAAAIMAIALANGNGK	92
SEQIDNO2	249	248
StPHA2	93 PFDWQDFVGIVCLLVINSTISFIEENNAGNAAAAIMAGLAPKTKVLRDGR	142
SEQIDNO2	249	248
StPHA2	143 WSEQRAAILVPGDIISVKLGDIVPADARLLEGDPLKIDQSALTGESLPVT	192
SEQIDNO2	249	248
StPHA2	193 KNPGDEVFSGSTCKQGELEAVVIATGVHTFFGKAAHLVDSTNNVGHFQKV	212
SEQIDNO2	249	248
StPHA2	243 LTAIGNFCICSIAVGMLGBIIVMYPIQHRKYRDGIDNLLVLLIGGIPIAM	292
SEQIDNO2	249	248

```
StPHA2      293 PIVLSVIMAIGSHRLSQQGAITKRMTAIEEMAGMDVLCSDKTGTLTLNKL    342
SEQIDNO2    249                                                        248

StPHA2      343 SVDKTLVEVPVKCVDKEYVLLLPARASRVENQDAIDACMVGMLADPKEAR    392
SEQIDNO2    249                                                        248

StPHA2      393 AGIREVHELPFNPVDKRTALTYIDNNGNWHRASKGAPEQILDLCNCKEDV    442
SEQIDNO2    249                                                        248

StPHA2      443 RRKVHSMIDKYAEAGLRSLAVARQEVPRKSKESACCPWQFVGLLPLFDPP    492
SEQIDNO2    249                                                        248

StPHA2      493 RHDSAETIRRALNLGVNVKMITGDQLAIAKETCRRLGMGTNMYPSASLLG    542
SEQIDNO2    249                                                        248

StPHA2      543 QDKDSSIASLPVEELIEKADGFAGVFPEHKYEIVKKLQERKHIVGMTGDG    592
SEQIDNO2    249                                                        248

StPHA2      593 VNDAPALKKADIGIAVADATDAARGASDIVLTEPGLSVIIGAVLTSRAIF    642
SEQIDNO2    249                                                        248

StPHA2      643 QRMKNYTIYAVSITIRIVFGFMLIALIWKFDFSAFMVLIIAILNDGTIMT    692
SEQIDNO2    249                                                        248

StPHA2      693 ISKDRVKPSPMPDSWKLNEIFATCVVLGGYQALMTVLFFWAMHDTKFFSD    742
SEQIDNO2    249                                                        248

StPHA2      743 KFGVKDIRESDREMMSALYLQVSIISQALIFVTKSRSWSFVERPGALLMI    792
SEQIDNO2    249                                                        248

StPHA2      793 AFLIAQLVATLIAVYADWTFARVKGCGWGWAGVIWIFSIVTYFPLDIMKF    842
SEQIDNO2    249                                                        248

StPHA2      843 AIRYILSGKAWNNLLDNKTAPTTKKDYGKEEREAQWALAQRTLHGLQPPE    892
SEQIDNO2    249                                                        248

StPHA2      893 ASNLFNEKNSYRELSETAPQAKRRAEMARLRELITLKGHVESVVKLKGLD    942
SEQIDNO2    249                  248

StPHA2      943 IETIQQHYTV    952
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